

FIG. 1

SEQ ID NO: 1 HUMAN RAGE PARTIAL CODING SEQUENCE GenBank/EMBL Accession
No. M91211

1 ggggcagccg gaacagcagt tggagcctgg gtgctggtcc tcagtctgtg gggggcagta
61 gtaggtgctc aaaacatcac agcccggatt ggcgagccac tggtgctgaa gtgaagggg
121 gcccccaaga aaccaccca gcggttgaa tggaaactga acacaggccg gacagaagct
181 tggaaagtcc tgtctccca gggaggagc cctgggaca gtgtggctcg tgccttccc
241 aacggctccc tcttcttc ggctgctgg atccaggatg aggggatttt ccggtgcagg
301 gcaatgaaca ggaatggaaa ggagaccaag tccaactacc gagtccgtgt ctaccagatt
361 cctgggaagc cagaaattgt agattctgcc tctgaactca cggctggtgt tccaataag
421 gtggggacat gtgtgtcaga gggaagctac cctgcaggga ctcttagctg gcacttggat
481 ggggaagcccc tggtcctaa tgagaaggga gtatctgtga aggaacagac caggagacac
541 cctgagacag ggctcttcac actgcagtcg gagctaattg tgacccagc ccggggagga
601 gatccccgtc ccaccttctc ctgtagcttc agcccaggcc ttccccgaca ccgggccttg
661 cgcacagccc ccatccagcc ccgtgtctgg gagcctgtgc ctctggagga ggtccaattg
721 gtggtggagc cagaagggtg agcagtagct cctggtggaa ccgtaaccct gacctgtgaa
781 gtcctgtccc agccctctcc tcaaattcac tggatgaagg atggtgtgcc ctgtcccctt
841 cccccagcc ctgtgtgat cctccctgag atagggcctc aggaccaggg aacctacagc
901 tgtgtggcca ccattccag ccacgggccc caggaaagcc gtgctgtcag catcagcatc
961 atcgaaccag gcgaggagg gccaactgca ggctctgtgg gaggatcagg gctgggaact
1021 ctagccctgg ccctggggat cctgggagc ctggggacag ccgcccgtct cattggggtc
1081 atcttgtggc aaaggcggca acgcccagga gaggagagga aggcccaga aaaccaggag
1141 gaagaggagg agcgtgcaga actgaatcag tcggaggaac ctgaggcagg cgagagtagt
1201 actggagggc ctgaggggc ccacagacag atcccatcca tcagctcctt ttctttttc
1261 ccttgaactg ttctggcctc agaccaactc tctcctgtat aatctctctc ctgtataacc
1321 ccaccttgc aagctttct ctacaaccag agccccccac aatgatgatt aaacacctga
1381 cacatcttc a

FIG. 2A

atg gca gcc gga aca gca gtt gga gcc tgg gtg ctg gtc ctc agt ctg	48	SEQ ID NO: 2
Met Ala Ala Gly Thr Ala Val Gly Ala Trp Val Leu Val Leu Ser Leu		SEQ ID NO: 3
1 5 10 15		
tgg ggg gca gta gta ggt gct caa aac atc aca gcc cgg att ggc gag	96	
Trp Gly Ala Val Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu		
20 25 30		
cca ctg gtg ctg aag tgt aag ggg gcc ccc aag aaa cca ccc cag cgg	144	
Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg		
35 40 45		
ctg gaa tgg aaa ctg aac aca ggc cgg aca gaa gct tgg aag gtc ctg	192	
Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu		
50 55 60		
tct ccc cag gga gga ggc ccc tgg gac agt gtg gct cgt gtc ctt ccc	240	
Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro		
65 70 75 80		
aac ggc tcc ctc ttc ctt ccg gct gtc ggg atc cag gat gag ggg att	288	
Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile		
85 90 95		
ttc cgg tgc cag gca atg aac agg aat gga aag gag acc aag tcc aac	336	
Phe Arg Cys Gln Ala Met Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn		
100 105 110		
tac cga gtc cgt gtc tac cag att cct ggg aag cca gaa att gta gat	384	
Tyr Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp		
115 120 125		
tct gcc tct gaa ctc acg gct ggt gtt ccc aat aag gtg ggg aca tgt	432	
Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr Cys		
130 135 140		
gtg tca gag gga agc tac cct gca ggg act ctt agc tgg cac ttg gat	480	
Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp		
145 150 155 160		
ggg aag ccc ctg gtg cct aat gag aag gga gta tct gtg aag gaa cag	528	
Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln		
165 170 175		
acc agg aga cac cct gag aca ggg ctc ttc aca ctg cag tcg gag cta	576	
Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu		
180 185 190		
atg gtg acc cca gcc cgg gga gga gat ccc cgt ccc acc ttc tcc tgt	624	
Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys		
195 200 205		
agc ttc agc cca ggc ctt ccc cga cac cgg gcc ttg cgc aca gcc ccc	672	
Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro		
210 215 220		
atc cag ccc cgt gtc tgg gag cct gtg cct ctg gag gag gtc caa ttg	720	
Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu		
225 230 235 240		
gtg gtg gag cca gaa ggt gga gca gta gct cct ggt gga acc gta acc	768	
Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr		
245 250 255		
ctg acc tgt gaa gtc cct gcc cag ccc tct cct caa atc cac tgg atg	816	
Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met		
260 265 270		
aag gat ggt gtg ccc ttg ccc ctt ccc ccc agc cct gtg ctg atc ctc	864	
Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu		
275 280 285		
cct gag ata ggg cct cag gac cag gga acc tac agc tgt gtg gcc acc	912	
Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr		
290 295 300		
cat tcc agc cac ggg ccc cag gaa agc cgt gct gtc agc atc agc atc	960	
His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile		
305 310 315 320		
atc gaa cca ggc gag gag ggg cca act gca ggc tct gtg gga gga tca	1008	
Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser		
325 330 335		
ggg ctg gtc tag	1020	
Gly Leu Val		

FIG. 2B

SEQ ID NO: 4 HUMAN RAGE V-DOMAIN

gctc aaaacatcac agcccgatt ggcgagccac tgggtgctgaa gtgtaagggg
gcccccaaga aaccaccca gcggctggaa tggaaactga acacaggccg gacagaagct
tggaaggctc tgtctccca gggaggaggc cctgggaca gtgtggctcg tgccttccc
aacggctccc tctcctcc ggctgtcggg atccaggatg aggggatttt ccggtgcagg
gcaatgaaca ggaatggaaa ggagaccaag tccaactacc gagtccgtgt ctaccagatt
cctgggaagc cagaaattgt agattctgcc tctgaactca cg

FIG. 2C

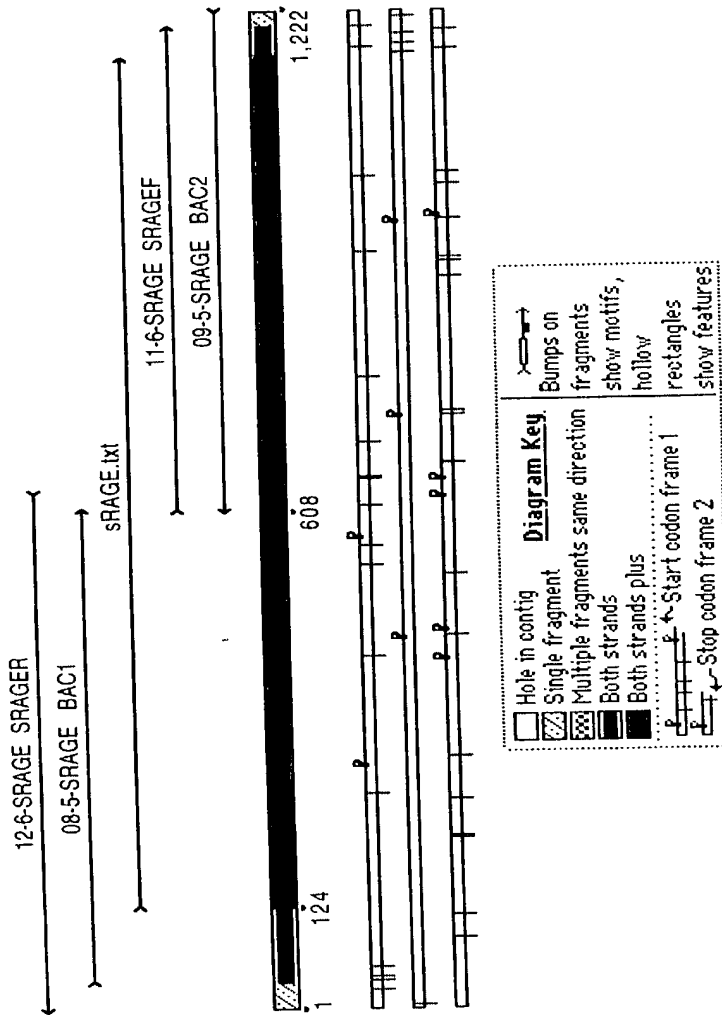


Fig. 3

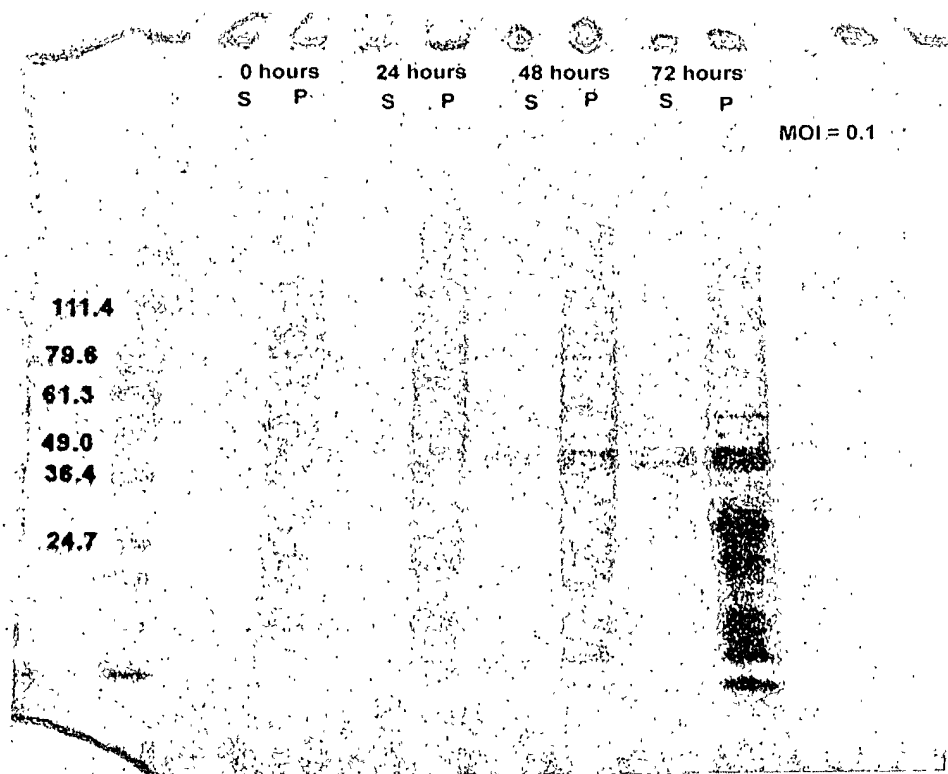


FIG. 4